

Resource Summary Report

Generated by [RRID](#) on Aug 6, 2026

[MAPPOP](#)

RRID:SCR_013490

Type: Tool

Proper Citation

MAPPOP (RRID:SCR_013490)

Resource Information

URL: <http://www.bio.unc.edu/faculty/vision/lab/mappop/>

Proper Citation: MAPPOP (RRID:SCR_013490)

Description: Software application that selects high resolution mapping subsamples and performs bin mapping (entry from Genetic Analysis Software)

Abbreviations: MAPPOP

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, matlab, unix, ms-windows, macos, etc

Resource Name: MAPPOP

Resource ID: SCR_013490

Alternate IDs: nlx_154467

Record Creation Time: 20220129T080316+0000

Record Last Update: 20260805T044313+0000

Ratings and Alerts

No rating or validation information has been found for MAPPOP.

No alerts have been found for MAPPOP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#) .

Cuevas HE, et al. (2021) The inheritance of anthracnose (*Colletotrichum sublineola*) resistance in sorghum differential lines QL3 and IS18760. *Scientific reports*, 11(1), 20525.

Cruet-Burgos CM, et al. (2020) Genomic Dissection of Anthracnose (*Colletotrichum sublineolum*) Resistance Response in Sorghum Differential Line SC112-14. *G3* (Bethesda, Md.), 10(4), 1403.

Wagner G, et al. (2019) Resolution of quantitative resistance to clubroot into QTL-specific metabolic modules. *Journal of experimental botany*, 70(19), 5375.

Boutet G, et al. (2016) SNP discovery and genetic mapping using genotyping by sequencing of whole genome genomic DNA from a pea RIL population. *BMC genomics*, 17, 121.

Finkers-Tomczak A, et al. (2011) Comparative sequence analysis of the potato cyst nematode resistance locus H1 reveals a major lack of co-linearity between three haplotypes in potato (*Solanum tuberosum* ssp.). *TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik*, 122(3), 595.